

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 15:59:05 ; Search time 29.5 Seconds
 (without alignments)
 92.993 Million cell updates/sec

Title: US-10-519-890-10

Perfect score: 32

Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%				
No.	Score	Match	Length	DB	ID	Description
1	32	100.0	6	8	ADI29056	Adi29056 Human ins
2	32	100.0	154	4	ABB64396	Abb64396 Drosophil
3	32	100.0	198	3	AAG27975	Aag27975 Arabidops
4	32	100.0	305	3	AAG30828	Aag30828 Arabidops
5	32	100.0	316	3	AAG27974	Aag27974 Arabidops
6	32	100.0	332	3	AAG30827	Aag30827 Arabidops
7	32	100.0	343	3	AAG27973	Aag27973 Arabidops
8	32	100.0	366	3	AAG30826	Aag30826 Arabidops
9	32	100.0	377	3	AAG27972	Aag27972 Arabidops
10	32	100.0	530	4	ABG29689	Abg29689 Novel hum
11	32	100.0	708	4	ABB58681	Abb58681 Drosophil
12	30	93.8	10	6	ABU52535	Abu52535 Peanut Ar

13	30	93.8	457	6	ADA33529	Ada33529	Acinetoba
14	30	93.8	1653	4	AAG98354	Aag98354	Escherich
15	30	93.8	1653	9	AED82056	Aed82056	Hyperimmu
16	30	93.8	1653	9	AED82491	Aed82491	Hyperimmu
17	29	90.6	28	8	ADF53701	Adf53701	Equine gh
18	29	90.6	28	8	ADL66842	Adl66842	Equine Gh
19	29	90.6	28	8	ADU61121	Adu61121	Equine gr
20	29	90.6	61	4	AAU44456	Aau44456	Propionib
21	29	90.6	61	6	ABM40975	Abm40975	Propionib
22	29	90.6	66	6	ABM65179	Abm65179	Propionib
23	29	90.6	79	4	ABG04784	Abg04784	Novel hum
24	29	90.6	86	6	ABM64707	Abm64707	Propionib
25	29	90.6	95	4	AAU40300	Aau40300	Propionib
26	29	90.6	95	6	ABM36819	Abm36819	Propionib
27	29	90.6	96	4	AAU64553	Aau64553	Propionib
28	29	90.6	96	6	ABM61072	Abm61072	Propionib
29	29	90.6	98	4	AAU59044	Aau59044	Propionib
30	29	90.6	98	6	ABM55563	Abm55563	Propionib
31	29	90.6	105	7	ADL06716	Adl06716	Human bra
32	29	90.6	105	7	ADL06714	Adl06714	Human bra
33	29	90.6	123	4	ABB15200	Abb15200	Human ner
34	29	90.6	127	4	ABG29587	Abg29587	Novel hum
35	29	90.6	145	7	ADE95986	Ade95986	Human uri
36	29	90.6	152	6	ABM64566	Abm64566	Propionib
37	29	90.6	156	4	AAU86633	Aau86633	Novel hum
38	29	90.6	156	7	ADB59967	Adb59967	Connectiv
39	29	90.6	158	6	ABR43445	Abr43445	Human mal
40	29	90.6	158	8	ADR46858	Adr46858	Human cys
41	29	90.6	159	6	ABU36844	Abu36844	Protein e
42	29	90.6	159	6	ABU34765	Abu34765	Protein e
43	29	90.6	165	3	AAB56382	Aab56382	Human pro
44	29	90.6	167	4	AAU31752	Aau31752	Novel hum
45	29	90.6	175	7	ABO84199	Abo84199	Pseudomon
46	29	90.6	181	2	AAW70986	Aaw70986	Amino aci
47	29	90.6	181	6	ABU33879	Abu33879	Protein e
48	29	90.6	181	8	ADS75085	Ads75085	M. avium
49	29	90.6	202	9	AEA04765	Aea04765	Indian he
50	29	90.6	211	7	ABO68295	Abo68295	Pseudomon
51	29	90.6	227	7	ABO71888	Abo71888	Pseudomon
52	29	90.6	238	9	ABM93884	Abm93884	M. xanthu
53	29	90.6	248	7	ABO80503	Abo80503	Pseudomon
54	29	90.6	258	7	ABO74247	Abo74247	Pseudomon
55	29	90.6	269	9	AEC64310	Aec64310	Poplar SG
56	29	90.6	272	8	ADT58322	Adt58322	Plant pol
57	29	90.6	301	8	ADX92889	Adx92889	Plant ful
58	29	90.6	312	7	ABO82458	Abo82458	Pseudomon
59	29	90.6	316	8	ADN26248	Adn26248	Bacterial
60	29	90.6	326	7	ABO76724	Abo76724	Pseudomon
61	29	90.6	326	8	ABO58549	Abo58549	Human gen
62	29	90.6	335	8	ADY11082	Ady11082	Plant ful
63	29	90.6	349	4	ABB62556	Abb62556	Drosophil
64	29	90.6	350	7	ABO77322	Abo77322	Pseudomon
65	29	90.6	365	8	ADY09180	Ady09180	Plant ful
66	29	90.6	367	8	ADO51711	Ado51711	Streptomy
67	29	90.6	386	7	ABO70481	Abo70481	Pseudomon
68	29	90.6	388	6	AAE32782	Aae32782	Mycobacte
69	29	90.6	392	4	ABG25625	Abg25625	Novel hum
70	29	90.6	392	4	ABG25990	Abg25990	Novel hum
71	29	90.6	392	4	ABG25082	Abg25082	Novel hum
72	29	90.6	398	8	ADX79724	Adx79724	Plant ful
73	29	90.6	411	2	AAW94474	Aaw94474	Human Ihh

74	29	90.6	411	2	AY05860	Aay05860 Human Ind
75	29	90.6	411	2	AAW97763	Aaw97763 Human Ind
76	29	90.6	411	2	AY05516	Aay05516 Human Ind
77	29	90.6	411	3	AY96249	Aay96249 Human Ihh
78	29	90.6	411	3	AY70682	Aay70682 Human Ind
79	29	90.6	411	3	AY95287	Aay95287 Human Ind
80	29	90.6	411	3	AY95978	Aay95978 Human Ind
81	29	90.6	411	4	AAB84675	Aab84675 Amino aci
82	29	90.6	411	4	AAB60266	Aab60266 Human Ind
83	29	90.6	411	4	AAE04688	Aae04688 Human ind
84	29	90.6	411	4	AAB85091	Aab85091 Human ind
85	29	90.6	411	4	AAG65749	Aag65749 Human ind
86	29	90.6	411	5	AAE14298	Aae14298 Human Ind
87	29	90.6	411	5	AAO20924	Aao20924 Human Ihh
88	29	90.6	411	5	AAU99484	Aau99484 Human Ind
89	29	90.6	411	7	ADK66382	Adk66382 Human ind
90	29	90.6	411	7	ADL06710	Adl06710 Human bra
91	29	90.6	411	7	ADL06712	Adl06712 Human bra
92	29	90.6	411	8	ADH56644	Adh56644 Human Ind
93	29	90.6	411	8	ADK82143	Adk82143 Human Ind
94	29	90.6	411	8	ADR03323	Adr03323 Human Ind
95	29	90.6	411	9	ADU81698	Adu81698 Human Ind
96	29	90.6	411	9	ADZ72181	Adz72181 Human ind
97	29	90.6	411	9	ADZ76232	Adz76232 Human Ind
98	29	90.6	411	9	AEB22478	Aeb22478 Human Ind
99	29	90.6	411	9	AED67915	Aed67915 Human ind
100	29	90.6	411	10	AEE84665	Aee84665 Indian he
101	29	90.6	413	5	ABG91520	Abg91520 Purine/py
102	29	90.6	413	8	ADS43190	Ads43190 Bacterial
103	29	90.6	416	4	AAB96271	Aab96271 Putative
104	29	90.6	426	4	AAU42357	Aau42357 Propionib
105	29	90.6	426	6	ABM38876	Abm38876 Propionib
106	29	90.6	430	3	AAG49406	Aag49406 Arabidops
107	29	90.6	436	7	ABO72128	Abo72128 Pseudomon
108	29	90.6	437	8	ADN73531	Adn73531 Thale cre
109	29	90.6	438	8	ADY07348	Ady07348 Plant ful
110	29	90.6	446	3	AAG49405	Aag49405 Arabidops
111	29	90.6	452	3	AAG49404	Aag49404 Arabidops
112	29	90.6	456	7	ABO81779	Abo81779 Pseudomon
113	29	90.6	473	7	ABO76296	Abo76296 Pseudomon
114	29	90.6	498	8	ADX93481	Adx93481 Plant ful
115	29	90.6	553	7	ABO83875	Abo83875 Pseudomon
116	29	90.6	568	7	ABO74518	Abo74518 Pseudomon
117	29	90.6	568	7	ABO78805	Abo78805 Pseudomon
118	29	90.6	574	7	ABO70709	Abo70709 Pseudomon
119	29	90.6	589	6	ABU35784	Abu35784 Protein e
120	29	90.6	605	7	ABO70716	Abo70716 Pseudomon
121	29	90.6	608	4	AAG91551	Aag91551 C glutami
122	29	90.6	626	4	ABB64471	Abb64471 Drosophil
123	29	90.6	647	8	ADU01120	Adu01120 Human pro
124	29	90.6	647	8	ADU15502	Adu15502 Novel hum
125	29	90.6	672	7	ABO68195	Abo68195 Pseudomon
126	29	90.6	682	7	ABO74251	Abo74251 Pseudomon
127	29	90.6	705	7	ABO79607	Abo79607 Pseudomon
128	29	90.6	726	4	ABB64481	Abb64481 Drosophil
129	29	90.6	827	7	ADF55472	Adf55472 Human nov
130	29	90.6	846	4	ABG11594	Abg11594 Novel hum
131	29	90.6	852	6	AAO30995	Aao30995 Human tra
132	29	90.6	871	7	AEB86062	Aeb86062 Protein d
133	29	90.6	1008	7	ABO80673	Abo80673 Pseudomon
134	29	90.6	1020	7	ABO80124	Abo80124 Pseudomon

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:44 ; Search time 6.25 Seconds
 (without alignments)
 92.368 Million cell updates/sec

Title: US-10-519-890-10

Perfect score: 32

Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query					Description
		Match	Length	DB	ID		
1	32	100.0	259	2	G82601		conserved hypothet
2	32	100.0	366	2	D96649		hypothetical prote
3	30	93.8	445	2	D84385		oligopeptide ABC t
4	30	93.8	493	2	T07911		catalase (EC 1.11.
5	30	93.8	1644	2	AC0823		probable lipoprote
6	30	93.8	1653	2	B91052		hypothetical prote
7	30	93.8	1653	2	F85896		hypothetical prote
8	30	93.8	1653	2	G65028		hypothetical prote
9	29	90.6	118	2	D72609		hypothetical prote
10	29	90.6	159	2	B70881		probable dfrA prot
11	29	90.6	225	2	A75425		hypothetical prote
12	29	90.6	388	2	G70729		hypothetical prote
13	29	90.6	413	2	H75070		sugar-phosphate nu
14	29	90.6	423	2	T05396		hypothetical prote
15	29	90.6	423	2	T05343		hypothetical prote
16	29	90.6	431	2	T33287		hypothetical prote
17	29	90.6	475	2	T36921		hypothetical prote
18	29	90.6	482	2	G70063		cardiolipin synth

19	29	90.6	589	1	S42047	aspartate-tRNA lig
20	29	90.6	901	2	T20122	hypothetical prote
21	29	90.6	928	2	T24868	hypothetical prote
22	29	90.6	1207	2	T00378	KIAA0641 protein -
23	29	90.6	2109	2	I38414	transcription fact
24	29	90.6	2670	2	T37919	GCN1 homolog - fis
25	28	87.5	117	1	A59316	ghrelin precursor
26	28	87.5	117	1	B59316	ghrelin precursor
27	28	87.5	143	2	S63735	HIV-1 retropepsin
28	28	87.5	424	1	B40905	inhibin beta-A cha
29	28	87.5	424	1	S31440	inhibin beta-A cha
30	28	87.5	424	1	WFPGBA	inhibin beta-A cha
31	28	87.5	425	1	S50898	inhibin beta-A cha
32	28	87.5	425	2	I47072	inhibin beta-A cha
33	28	87.5	426	1	B24248	inhibin beta-A cha
34	28	87.5	452	2	JC4100	hydroxyindole O-me
35	28	87.5	540	2	A75250	carboxylesterase,
36	28	87.5	547	2	E70720	probable ilvG prot
37	28	87.5	565	2	T08794	hypothetical prote
38	28	87.5	600	2	D83430	type III secretion
39	28	87.5	755	2	B75346	probable competenc
40	28	87.5	772	2	H86492	Pmp_3 [imported] -
41	28	87.5	855	2	C82983	hypothetical prote
42	28	87.5	1039	2	T35878	hypothetical prote
43	28	87.5	1123	2	T47687	adaptor protein/ a
44	28	87.5	1260	2	A86323	protein F14D16.3 [
45	28	87.5	1426	2	A99580	hypothetical prote
46	28	87.5	1846	2	T33079	hypothetical prote
47	28	87.5	2247	2	T16637	hypothetical prote
48	27	84.4	50	4	IMBP13	hypothetical immun
49	27	84.4	107	1	WMLJSP	S1 protein - human
50	27	84.4	121	2	T08717	hypothetical prote
51	27	84.4	127	2	I57612	hypothetical prote
52	27	84.4	127	2	T14797	hypothetical prote
53	27	84.4	142	2	G86398	protein F17L21.8 [
54	27	84.4	154	2	E64504	hypothetical prote
55	27	84.4	193	2	A33562	pol polyprotein -
56	27	84.4	210	2	T41082	probable mitochond
57	27	84.4	231	2	D75412	hypothetical prote
58	27	84.4	270	2	JC7631	K+ channel-interac
59	27	84.4	304	2	A33274	insulin-like growt
60	27	84.4	305	2	JN0508	insulin-like growt
61	27	84.4	305	2	I48601	insulin-like growt
62	27	84.4	310	2	A60967	insulin-like growt
63	27	84.4	317	2	I46916	insulin-like growt
64	27	84.4	328	1	A41927	insulin-like growt
65	27	84.4	334	1	T51050	probable phosphopr
66	27	84.4	353	2	H87545	vanillate O-demeth
67	27	84.4	353	2	A83609	probable periplasm
68	27	84.4	366	1	DEBSIC	3-isopropylmalate
69	27	84.4	391	2	T36739	hypothetical prote
70	27	84.4	402	2	T52522	hypothetical prote
71	27	84.4	404	2	F71324	probable gcpE prot
72	27	84.4	414	2	B98354	hypothetical prote
73	27	84.4	446	2	F69053	conserved hypothet
74	27	84.4	463	2	S28469	phosphomannomutase
75	27	84.4	467	2	T01462	hypothetical prote
76	27	84.4	492	2	AC0768	probable transmemb
77	27	84.4	502	2	T27908	hypothetical prote
78	27	84.4	520	2	H64510	hypothetical prote
79	27	84.4	537	2	C71008	probable proline p

80	27	84.4	595	2	T04438	hypothetical prote
81	27	84.4	609	2	F70512	probable ATPase -
82	27	84.4	609	2	S72845	H+-transporting tw
83	27	84.4	665	2	JC7191	85K c-Cbl-interact
84	27	84.4	700	2	A61527	stonustoxin beta c
85	27	84.4	705	2	T35165	probable integral
86	27	84.4	738	2	AB2899	primosomal protein
87	27	84.4	763	2	C97674	primosomal protein
88	27	84.4	779	2	G87573	xanthine dehydroge
89	27	84.4	789	1	B4AGA6	virB4 protein prec
90	27	84.4	793	2	S67070	GAC1 protein - yea
91	27	84.4	825	2	AC0039	glycerol-3-phospha
92	27	84.4	844	2	F86231	hypothetical prote
93	27	84.4	970	2	E70533	probable sulfatase
94	27	84.4	1056	2	G84865	hypothetical prote
95	27	84.4	1083	1	S53048	alpha-mannosidase
96	27	84.4	1157	1	GNLJLK	pol polyprotein -
97	27	84.4	1161	2	S18738	pol protein - simi
98	27	84.4	1293	2	S42402	xeroderma pigmento
99	27	84.4	1303	2	E96805	hypothetical prote
100	27	84.4	1336	2	T17479	hypothetical prote
101	27	84.4	1830	1	S19188	myosin-V - chicken
102	27	84.4	2314	2	T28698	hypothetical prote
103	27	84.4	2342	2	T13412	hypothetical prote
104	27	84.4	2531	2	T16743	hypothetical prote
105	27	84.4	3161	2	T30342	protein HMWP1 - Ye
106	27	84.4	5126	2	S40450	ryanodine receptor
107	26	81.2	82	2	T10149	probable hexose tr
108	26	81.2	112	2	D72654	hypothetical prote
109	26	81.2	114	2	E70757	hypothetical prote
110	26	81.2	116	2	D97573	hypothetical prote
111	26	81.2	124	2	B45945	histone H2B - rat
112	26	81.2	125	2	S26185	histone H2B - rat
113	26	81.2	131	2	S42592	urease (EC 3.5.1.5
114	26	81.2	134	2	T12584	asparagine synthas
115	26	81.2	150	2	T35638	hypothetical prote
116	26	81.2	161	2	S39483	ubiquitin-conjugat
117	26	81.2	183	2	C55663	oligodendrocyte-sp
118	26	81.2	214	2	D64442	conserved hypothet
119	26	81.2	232	2	B96803	hypothetical prote
120	26	81.2	235	2	G81138	probable succinate
121	26	81.2	237	2	AF0645	probable regulator
122	26	81.2	239	2	T36995	hypothetical prote
123	26	81.2	240	2	T35972	hypothetical prote
124	26	81.2	252	2	JC2399	PMS4 homolog misma
125	26	81.2	259	2	E82191	probable nicotinat
126	26	81.2	266	2	A86288	protein F9L1.30 [i
127	26	81.2	267	2	H84396	hypothetical prote
128	26	81.2	271	2	T36040	hypothetical prote
129	26	81.2	273	2	B99816	hypothetical prote
130	26	81.2	273	2	F85675	hypothetical prote
131	26	81.2	279	2	E64856	hypothetical prote
132	26	81.2	304	1	SYSPMG	dTDP-dihydrostrept
133	26	81.2	306	2	B97315	aldo/keto reductas
134	26	81.2	322	2	A70607	hypothetical prote
135	26	81.2	328	2	E81089	glucokinase (EC 2.
136	26	81.2	330	2	T22411	hypothetical prote
137	26	81.2	349	2	AB1715	oxidoreductase hom
138	26	81.2	349	2	AG1344	oxidoreductase hom
139	26	81.2	363	2	C44971	histidine-rich kno
140	26	81.2	364	2	A70474	conserved hypothet

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:03:03 ; Search time 11.5 Seconds
 (without alignments)
 45.668 Million cell updates/sec

Title: US-10-519-890-10

Perfect score: 32

Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	32	100.0	56	2	US-09-270-767-34420	Sequence 34420, A
2	32	100.0	56	2	US-09-270-767-49637	Sequence 49637, A
3	32	100.0	182	2	US-09-270-767-43696	Sequence 43696, A
4	30	93.8	457	2	US-09-328-352-4816	Sequence 4816, Ap
5	29	90.6	147	2	US-09-270-767-58356	Sequence 58356, A
6	29	90.6	175	2	US-09-252-991A-32945	Sequence 32945, A
7	29	90.6	181	2	US-08-990-791-2	Sequence 2, Appli
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133	28	87.5	28	4	US-10-276-392-16	Sequence 16, Appl
134	28	87.5	28	4	US-10-276-392-17	Sequence 17, Appl
135	28	87.5	28	4	US-10-276-392-18	Sequence 18, Appl
136	28	87.5	28	4	US-10-276-392-19	Sequence 19, Appl
137	28	87.5	28	4	US-10-276-392-20	Sequence 20, Appl
138	28	87.5	28	4	US-10-276-392-21	Sequence 21, Appl

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:04:43 ; Search time 3.5 Seconds
 (without alignments)
 45.998 Million cell updates/sec

Title: US-10-519-890-10
 Perfect score: 32
 Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	29	90.6	86	6	US-10-953-349-40084	Sequence 40084, A
2	29	90.6	131	6	US-10-449-902-47275	Sequence 47275, A
3	29	90.6	153	6	US-10-953-349-25819	Sequence 25819, A
4	29	90.6	175	6	US-10-953-349-25818	Sequence 25818, A
5	29	90.6	318	6	US-10-953-349-26735	Sequence 26735, A
6	29	90.6	344	6	US-10-449-902-50913	Sequence 50913, A
7	29	90.6	686	6	US-10-449-902-45827	Sequence 45827, A
8	28	87.5	28	7	US-11-257-498-33	Sequence 33, Appl
9	28	87.5	28	7	US-11-257-498-34	Sequence 34, Appl
10	28	87.5	28	7	US-11-257-498-35	Sequence 35, Appl
11	28	87.5	28	7	US-11-257-498-40	Sequence 40, Appl
12	28	87.5	117	7	US-11-255-699-6	Sequence 6, Appl
13	28	87.5	121	7	US-11-356-823-21	Sequence 21, Appl
14	28	87.5	341	6	US-10-953-349-31800	Sequence 31800, A

15	28	87.5	377	6	US-10-953-349-31798	Sequence 31798, A
16	28	87.5	388	6	US-10-953-349-32611	Sequence 32611, A
17	28	87.5	555	7	US-11-293-697-4766	Sequence 4766, Ap
18	28	87.5	755	6	US-10-449-902-47527	Sequence 47527, A
19	27	84.4	38	6	US-10-449-902-29624	Sequence 29624, A
20	27	84.4	38	6	US-10-449-902-34229	Sequence 34229, A
21	27	84.4	75	6	US-10-953-349-10327	Sequence 10327, A
22	27	84.4	160	6	US-10-449-902-45257	Sequence 45257, A
23	27	84.4	209	6	US-10-449-902-37987	Sequence 37987, A
24	27	84.4	291	6	US-10-449-902-52072	Sequence 52072, A
25	27	84.4	311	6	US-10-449-902-36921	Sequence 36921, A
26	27	84.4	311	6	US-10-449-902-47134	Sequence 47134, A
27	27	84.4	328	6	US-10-505-928-191	Sequence 191, App
28	27	84.4	338	7	US-11-174-307B-3180	Sequence 3180, Ap
29	27	84.4	352	7	US-11-174-307B-3460	Sequence 3460, Ap
30	27	84.4	599	7	US-11-293-697-3692	Sequence 3692, Ap
31	27	84.4	622	6	US-10-449-902-54041	Sequence 54041, A
32	27	84.4	710	6	US-10-449-902-55139	Sequence 55139, A
33	27	84.4	751	6	US-10-449-902-55410	Sequence 55410, A
34	27	84.4	1164	7	US-11-294-155-8	Sequence 8, Appli
35	27	84.4	1202	7	US-11-294-155-22	Sequence 22, Appli
36	26	81.2	47	7	US-11-116-142B-12	Sequence 12, Appli
37	26	81.2	112	6	US-10-953-349-16419	Sequence 16419, A
38	26	81.2	161	6	US-10-953-349-27684	Sequence 27684, A
39	26	81.2	161	6	US-10-449-902-56689	Sequence 56689, A
40	26	81.2	180	6	US-10-953-349-27683	Sequence 27683, A
41	26	81.2	185	6	US-10-953-349-39035	Sequence 39035, A
42	26	81.2	192	6	US-10-953-349-39034	Sequence 39034, A
43	26	81.2	198	6	US-10-449-902-34937	Sequence 34937, A
44	26	81.2	204	7	US-11-293-697-4233	Sequence 4233, Ap
45	26	81.2	216	6	US-10-953-349-33317	Sequence 33317, A
46	26	81.2	246	6	US-10-449-902-51236	Sequence 51236, A
47	26	81.2	250	7	US-11-293-697-4069	Sequence 4069, Ap
48	26	81.2	259	6	US-10-953-349-33316	Sequence 33316, A
49	26	81.2	261	6	US-10-449-902-31054	Sequence 31054, A
50	26	81.2	261	6	US-10-449-902-52282	Sequence 52282, A
51	26	81.2	293	6	US-10-449-902-30804	Sequence 30804, A
52	26	81.2	308	6	US-10-953-349-26114	Sequence 26114, A
53	26	81.2	310	6	US-10-449-902-31942	Sequence 31942, A
54	26	81.2	310	6	US-10-449-902-45792	Sequence 45792, A
55	26	81.2	337	6	US-10-953-349-39284	Sequence 39284, A
56	26	81.2	339	6	US-10-953-349-34788	Sequence 34788, A
57	26	81.2	357	6	US-10-449-902-49470	Sequence 49470, A
58	26	81.2	362	6	US-10-953-349-33315	Sequence 33315, A
59	26	81.2	363	6	US-10-449-902-43360	Sequence 43360, A
60	26	81.2	364	6	US-10-953-349-26113	Sequence 26113, A
61	26	81.2	369	6	US-10-953-349-28327	Sequence 28327, A
62	26	81.2	379	6	US-10-449-902-48349	Sequence 48349, A
63	26	81.2	384	7	US-11-293-697-2595	Sequence 2595, Ap
64	26	81.2	395	6	US-10-953-349-26112	Sequence 26112, A
65	26	81.2	400	6	US-10-953-349-28326	Sequence 28326, A
66	26	81.2	401	6	US-10-953-349-35747	Sequence 35747, A
67	26	81.2	403	6	US-10-449-902-48024	Sequence 48024, A
68	26	81.2	431	6	US-10-953-349-35746	Sequence 35746, A
69	26	81.2	435	7	US-11-174-307B-3160	Sequence 3160, Ap
70	26	81.2	445	6	US-10-449-902-45173	Sequence 45173, A
71	26	81.2	462	6	US-10-953-349-35745	Sequence 35745, A
72	26	81.2	464	6	US-10-449-902-48010	Sequence 48010, A
73	26	81.2	499	6	US-10-449-902-44934	Sequence 44934, A
74	26	81.2	501	6	US-10-449-902-37975	Sequence 37975, A
75	26	81.2	572	6	US-10-449-902-37842	Sequence 37842, A

76	26	81.2	661	6	US-10-449-902-42670	Sequence 42670, A
77	26	81.2	681	7	US-11-258-767-13	Sequence 13, Appl
78	26	81.2	695	7	US-11-258-767-26	Sequence 26, Appl
79	26	81.2	707	7	US-11-258-767-14	Sequence 14, Appl
80	26	81.2	707	7	US-11-258-767-20	Sequence 20, Appl
81	26	81.2	708	7	US-11-258-767-16	Sequence 16, Appl
82	26	81.2	708	7	US-11-258-767-19	Sequence 19, Appl
83	26	81.2	708	7	US-11-258-767-22	Sequence 22, Appl
84	26	81.2	708	7	US-11-258-767-23	Sequence 23, Appl
85	26	81.2	708	7	US-11-258-767-24	Sequence 24, Appl
86	26	81.2	708	7	US-11-258-767-28	Sequence 28, Appl
87	26	81.2	708	7	US-11-258-767-29	Sequence 29, Appl
88	26	81.2	708	7	US-11-258-767-32	Sequence 32, Appl
89	26	81.2	708	7	US-11-258-767-35	Sequence 35, Appl
90	26	81.2	708	7	US-11-258-767-38	Sequence 38, Appl
91	26	81.2	708	7	US-11-258-767-39	Sequence 39, Appl
92	26	81.2	709	7	US-11-258-767-31	Sequence 31, Appl
93	26	81.2	710	7	US-11-258-767-33	Sequence 33, Appl
94	26	81.2	711	7	US-11-258-767-12	Sequence 12, Appl
95	26	81.2	711	7	US-11-258-767-15	Sequence 15, Appl
96	26	81.2	711	7	US-11-258-767-17	Sequence 17, Appl
97	26	81.2	711	7	US-11-258-767-18	Sequence 18, Appl
98	26	81.2	711	7	US-11-258-767-21	Sequence 21, Appl
99	26	81.2	711	7	US-11-258-767-27	Sequence 27, Appl
100	26	81.2	711	7	US-11-258-767-30	Sequence 30, Appl
101	26	81.2	711	7	US-11-258-767-34	Sequence 34, Appl
102	26	81.2	720	6	US-10-505-928-383	Sequence 383, App
103	26	81.2	761	6	US-10-449-902-55285	Sequence 55285, A
104	26	81.2	777	6	US-10-449-902-54016	Sequence 54016, A
105	26	81.2	883	7	US-11-297-383-11	Sequence 11, Appl
106	26	81.2	1226	7	US-11-221-332-88	Sequence 88, Appl
107	26	81.2	1674	6	US-10-511-937-2587	Sequence 2587, Ap
108	25	78.1	21	6	US-10-781-841-52	Sequence 52, Appl
109	25	78.1	66	6	US-10-449-902-52748	Sequence 52748, A
110	25	78.1	74	6	US-10-953-349-28164	Sequence 28164, A
111	25	78.1	100	7	US-11-197-712-472	Sequence 472, App
112	25	78.1	105	6	US-10-449-902-53581	Sequence 53581, A
113	25	78.1	108	6	US-10-449-902-42732	Sequence 42732, A
114	25	78.1	109	7	US-11-197-712-471	Sequence 471, App
115	25	78.1	132	6	US-10-449-902-29137	Sequence 29137, A
116	25	78.1	132	6	US-10-449-902-48826	Sequence 48826, A
117	25	78.1	145	6	US-10-449-902-47086	Sequence 47086, A
118	25	78.1	163	6	US-10-953-349-15516	Sequence 15516, A
119	25	78.1	169	6	US-10-953-349-38494	Sequence 38494, A
120	25	78.1	195	6	US-10-449-902-29284	Sequence 29284, A
121	25	78.1	198	6	US-10-449-902-29924	Sequence 29924, A
122	25	78.1	198	6	US-10-449-902-48938	Sequence 48938, A
123	25	78.1	201	6	US-10-449-902-29726	Sequence 29726, A
124	25	78.1	206	6	US-10-953-349-35948	Sequence 35948, A
125	25	78.1	207	6	US-10-953-349-15515	Sequence 15515, A
126	25	78.1	219	6	US-10-370-959-43	Sequence 43, Appl
127	25	78.1	222	6	US-10-449-902-39894	Sequence 39894, A
128	25	78.1	233	6	US-10-953-349-35947	Sequence 35947, A
129	25	78.1	239	7	US-11-006-802-1	Sequence 1, Appli
130	25	78.1	239	7	US-11-006-802-5	Sequence 5, Appli
131	25	78.1	247	6	US-10-449-902-37903	Sequence 37903, A
132	25	78.1	249	6	US-10-449-902-47790	Sequence 47790, A
133	25	78.1	251	6	US-10-471-571A-1320	Sequence 1320, Ap
134	25	78.1	258	6	US-10-449-902-54726	Sequence 54726, A
135	25	78.1	266	7	US-11-174-307B-4916	Sequence 4916, Ap
136	25	78.1	268	6	US-10-953-349-16740	Sequence 16740, A

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:15 ; Search time 123.75 Seconds
 (without alignments)
 134.548 Million cell updates/sec

Title: US-10-519-890-16

Perfect score: 98

Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	93	94.9	141	2	Q5IF07_HORSE Q5if07 equus cabal
2	93	94.9	175	2	Q6LDF9_RAT Q6ldf9 rattus norv
3	93	94.9	304	1	IPB2_RAT P12843 rattus norv
4	93	94.9	304	2	Q569C7_RAT Q569c7 rattus norv
5	93	94.9	316	1	IPB2_PIG P24853 sus scrofa
6	93	94.9	317	1	IPB2_BOVIN P13384 bos taurus
7	93	94.9	317	1	IPB2_SHEEP Q29400 ovis aries
8	93	94.9	328	1	IPB2_HUMAN P18065 homo sapien
9	90	91.8	75	2	Q7T186_CHICK Q7t186 gallus gall
10	90	91.8	209	2	Q802T1_CHICK Q802t1 gallus gall
11	90	91.8	311	1	IPB2_CHICK P49705 gallus gall
12	87	88.8	304	2	Q9D057_MOUSE Q9d057 mus musculu
13	87	88.8	305	1	IPB2_MOUSE P47877 mus musculu
14	87	88.8	305	2	Q91VK7_MOUSE Q91vk7 mus musculu
15	75	76.5	281	2	Q5XHC5_XENLA Q5xhc5 xenopus lae
16	74	75.5	87	2	Q90ZR1_ORYLA Q90zr1 oryzae lat
17	74	75.5	271	2	Q4SM92_TETNG Q4sm92 tetraodon n
18	70	71.4	262	2	Q8JHX6_BRARE Q8jhx6 brachydanio
19	70	71.4	262	2	Q90YJ7_BRARE Q90yj7 brachydanio
20	70	71.4	276	1	IPB2_BRARE Q9pth3 brachydanio

21	69	70.4	283	2	Q3I344_ONCMY	Q3i344 oncorhynchus
22	67	68.4	286	2	Q8UVU5_SPAAU	Q8uvu5 sparus aura
23	61	62.2	145	2	Q9DFM6_GILMI	Q9dfm6 gillichthys
24	60	61.2	236	2	Q4SK70_TETNG	Q4sk70 tetraodon n
25	60	61.2	283	2	Q3I346_ONCMY	Q3i346 oncorhynchus
26	52	53.1	269	2	Q6PAX6_XENLA	Q6pax6 xenopus lae
27	52	53.1	390	2	Q3XR38_9PROT	Q3xr38 magnetococc
28	50	51.0	267	2	Q499C6_XENTR	Q499c6 xenopus tro
29	49	50.0	244	2	Q3HWG3_ONCMY	Q3hwg3 oncorhynchus
30	49	50.0	244	2	Q5GBG2_ONCTS	Q5gbg2 oncorhynchus
31	48	49.0	95	2	Q9GK34_SHEEP	Q9gk34 ovis aries
32	48	49.0	170	2	Q9ZHQ8_HELPY	Q9zhq8 helicobacte
33	48	49.0	199	2	Q9S609_HELPY	Q9s609 helicobacte
34	48	49.0	201	2	Q9ZIR8_HELPY	Q9zir8 helicobacte
35	48	49.0	205	2	Q9S608_HELPY	Q9s608 helicobacte
36	48	49.0	223	2	Q9ZHQ9_HELPY	Q9zhq9 helicobacte
37	48	49.0	234	2	Q9F7U4_HELPY	Q9f7u4 helicobacte
38	48	49.0	235	2	Q306Y7_HELPY	Q306y7 helicobacte
39	48	49.0	235	2	Q6PRE9_HELPY	Q6pre9 helicobacte
40	48	49.0	235	2	Q8KKD6_HELPY	Q8kkd6 helicobacte
41	48	49.0	236	2	Q48249_HELPY	Q48249 helicobacte
42	48	49.0	239	2	Q83Z34_HELPY	Q83z34 helicobacte
43	48	49.0	240	2	Q3LR56_HELPY	Q3lr56 helicobacte
44	48	49.0	252	2	Q68899_HELPY	Q68899 helicobacte
45	48	49.0	272	1	IBP1_RAT	P21743 rattus norv
46	48	49.0	272	2	Q5SVY8_MOUSE	Q5svy8 mus musculu
47	48	49.0	272	2	Q6Q484_SPETR	Q6q484 spermophilu
48	48	49.0	272	2	Q91WV8_MOUSE	Q91wv8 mus musculu
49	47	48.0	132	2	Q53VM7_PIG	Q53vm7 sus scrofa
50	47	48.0	262	1	IBP1_PIG	Q75zp3 sus scrofa
51	47	48.0	263	1	IBP1_BOVIN	P24591 bos taurus
52	47	48.0	263	2	Q2T9Z3_BOVIN	Q2t9z3 bos taurus
53	46	46.9	115	2	Q5IF08_HORSE	Q5if08 equus cabal
54	46	46.9	259	1	IBP1_HUMAN	P08833 homo sapien
55	46	46.9	259	2	Q6PEY6_HUMAN	Q6pey6 homo sapien
56	46	46.9	269	2	Q6PN72_CHICK	Q6pn72 gallus gall
57	46	46.9	291	2	Q4RMT3_TETNG	Q4rmt3 tetraodon n
58	46	46.9	358	2	Q3Q7C2_9GAMM	Q3q7c2 shewanella
59	45	45.9	272	1	IBP1_MOUSE	P47876 mus musculu
60	45	45.9	5317	2	Q8TA74_HEMPU	Q8ta74 hemicentrot
61	44	44.9	126	2	Q5Z3W4_NOCFA	Q5z3w4 nocardia fa
62	44	44.9	272	1	TRPA_LEGPA	Q5x5q1 legionella
63	44	44.9	272	1	TRPA_LEGPH	Q5zvy3 legionella
64	44	44.9	272	1	TRPA_LEGPL	Q5wx31 legionella
65	44	44.9	330	2	Q53LV6_ORYSA	Q53lv6 oryza sativ
66	44	44.9	358	2	Q33QD9_9GAMM	Q33qd9 shewanella
67	44	44.9	392	2	Q3QQL6_9RHOB	Q3qql6 silicibacte
68	44	44.9	393	2	Q5LMZ5_SILPO	Q5lmz5 silicibacte
69	44	44.9	596	2	Q8DIY3_SYNEL	Q8diy3 synechococc
70	44	44.9	1323	2	Q6BZ91_DEBHA	Q6bz91 debaryomyce
71	43	43.9	246	2	Q5LIJ9_BACFN	Q5lij9 bacteroides
72	43	43.9	246	2	Q64ZM3_BACFR	Q64zm3 bacteroides
73	43	43.9	352	2	Q8GSM4_LYCES	Q8gsm4 lycopersico
74	43	43.9	358	2	Q2WW93_9GAMM	Q2ww93 shewanella
75	43	43.9	358	2	Q2ZLP2_SHEPU	Q2zlp2 shewanella
76	43	43.9	364	2	Q613A9_CAEBR	Q613a9 caenorhabdi
77	43	43.9	407	2	Q2XH80_PSEPU	Q2xh80 pseudomonas
78	43	43.9	407	2	Q9R8R0_PSEPU	Q9r8r0 pseudomonas
79	43	43.9	407	2	Q3KFU8_PSEPF	Q3kfu8 pseudomonas
80	43	43.9	407	2	Q4KFY8_PSEF5	Q4kfy8 pseudomonas
81	43	43.9	407	2	Q88FB0_PSEPK	Q88fb0 pseudomonas

82	43	43.9	417	2	Q5V634_HALMA	Q5v634 haloarcula
83	43	43.9	425	2	Q4PJ71_9BACT	Q4pj71 uncultured
84	43	43.9	491	2	Q3VYJ0_9ACTO	Q3vyj0 frankia sp.
85	43	43.9	1358	2	Q4RWU3_TETNG	Q4rwu3 tetraodon n
86	43	43.9	1770	2	Q4VXC5_HUMAN	Q4vxc5 homo sapien
87	43	43.9	1783	2	Q4R9M7_HUMAN	Q4r9m7 homo sapien
88	43	43.9	1797	2	Q4R9M8_HUMAN	Q4r9m8 homo sapien
89	43	43.9	1809	2	Q4R9M9_HUMAN	Q4r9m9 homo sapien
90	43	43.9	1816	1	KIF1B_HUMAN	O60333 homo sapien
91	43	43.9	1816	2	Q4VXC6_HUMAN	Q4vxc6 homo sapien
92	43	43.9	1823	2	Q4VXC4_HUMAN	Q4vxc4 homo sapien
93	43	43.9	2086	2	Q4RVN7_TETNG	Q4rvn7 tetraodon n
94	43	43.9	2867	2	Q3M1N0_ANAVT	Q3m1n0 anabaena va
95	43	43.9	3035	2	O72347_9POTY	O72347 wheat strea
96	43	43.9	3035	2	Q8V1Y3_9POTY	Q8v1y3 wheat strea
97	42.5	43.4	203	2	Q3KJ29_PSEPF	Q3kj29 pseudomonas
98	42.5	43.4	328	2	Q61GN1_CAEBR	Q61gn1 caenorhabdi
99	42.5	43.4	601	2	Q7V0S7_PROMP	Q7v0s7 prochloroco
100	42.5	43.4	3302	2	Q6E7K0_9CYAN	Q6e7k0 lyngbya maj
101	42	42.9	146	2	Q7UML9_RHOBA	Q7uml9 rhodopirell
102	42	42.9	160	2	Q62L64_BURMA	Q62l64 burkholderi
103	42	42.9	286	2	Q84FA4_MYXXA	Q84fa4 myxococcus
104	42	42.9	334	2	Q9K9C0_BACHD	Q9k9c0 bacillus ha
105	42	42.9	372	2	Q3NLC7_SHEFR	Q3nlc7 shewanella
106	42	42.9	380	2	Q7MB58_PHOLL	Q7mb58 photorhabdu
107	42	42.9	406	2	Q48K70_PSE14	Q48k70 pseudomonas
108	42	42.9	406	2	Q883Z6_PSESM	Q883z6 pseudomonas
109	42	42.9	411	2	Q4ZUW9_PSEU2	Q4zuw9 pseudomonas
110	42	42.9	417	2	Q73KZ4_TREDE	Q73kz4 treponema d
111	42	42.9	592	2	Q4D1I2_TRYCR	Q4d1i2 trypanosoma
112	42	42.9	592	2	Q4PQV7_TRYCR	Q4pqv7 trypanosoma
113	42	42.9	604	2	Q4DB33_TRYCR	Q4db33 trypanosoma
114	42	42.9	741	2	Q6C6E3_YARLI	Q6c6e3 yarrowia li
115	42	42.9	764	2	Q4H3D3_CIOIN	Q4h3d3 ciona intes
116	42	42.9	890	2	Q4RHB2_TETNG	Q4rbh2 tetraodon n
117	42	42.9	1642	1	CO3_NAJKA	Q91132 naja kaouth
118	42	42.9	1652	2	Q49HM6_AUSSU	Q49hm6 austrelaps
119	41	41.8	50	2	Q5NLX0_ZYMMO	Q5nlx0 zymomonas m
120	41	41.8	123	2	Q8IEA5_PLAF7	Q8iea5 plasmodium
121	41	41.8	245	2	Q42A77_DESHA	Q42a77 desulfitoba
122	41	41.8	285	2	Q3APA2_CHLCH	Q3apa2 chlorobium
123	41	41.8	297	2	Q91RF1_9RHAB	Q91rf1 rabies viru
124	41	41.8	299	2	Q668J5_YERPS	Q668j5 yersinia ps
125	41	41.8	299	2	Q8ZCG6_YERPE	Q8zcg6 yersinia pe
126	41	41.8	304	2	Q8D0X2_YERPE	Q8d0x2 yersinia pe
127	41	41.8	307	2	Q6AF34_LEIXX	Q6af34 leifsonia x
128	41	41.8	315	2	Q74SG1_YERPE	Q74sg1 yersinia pe
129	41	41.8	324	2	Q7NNF8_GLOVI	Q7nnf8 gloeobacter
130	41	41.8	343	2	Q6D8W8_ERWCT	Q6d8w8 erwinia car
131	41	41.8	348	2	Q5KXQ7_GEOKA	Q5kxq7 geobacillus
132	41	41.8	349	2	Q43Q58_SOLUS	Q43q58 solibacter
133	41	41.8	358	2	Q8EA16_SHEON	Q8eai6 shewanella
134	41	41.8	384	1	GAL1_VIBF1	Q5e0ml vibrio fisc
135	41	41.8	390	2	O85598_BRUAB	O85598 brucella ab
136	41	41.8	392	2	Q3AC11_CARHZ	Q3ac11 carboxydoth
137	41	41.8	397	2	Q2YZN7_9DELT	Q2yzn7 uncultured
138	41	41.8	398	2	Q7RJ04_PLAYO	Q7rj04 plasmodium
139	41	41.8	401	2	Q59X24_CANAL	Q59x24 candida alb
140	41	41.8	419	2	Q4YUY2_PLABE	Q4yuy2 plasmodium
141	41	41.8	444	2	Q50ZU7_ENTHI	Q50zu7 entamoeba h
142	41	41.8	488	2	Q7NW11_CHRVO	Q7nw11 chromobacte

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OM protein - protein search, using sw model

Run on: July 10, 2006, 15:59:05 ; Search time 88.5 Seconds
 (without alignments)
 92.993 Million cell updates/sec

Title: US-10-519-890-16

Perfect score: 98

Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:
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 2: geneseqp1990s:
 3: geneseqp2000s:
 4: geneseqp2001s:
 5: geneseqp2002s:
 6: geneseqp2003as:
 7: geneseqp2003bs:
 8: geneseqp2004s:
 9: geneseqp2005s:
 10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	93	94.9	18	8	ADI29060	Adi29060 Human ins
4	93	94.9	23	8	ADI29051	Adi29051 Human ins
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6	93	94.9	36	3	AAB09735	Aab09735 IGFBP-2 I
7	93	94.9	37	3	AAB09736	Aab09736 IGFBP-2 I
8	93	94.9	39	3	AAB09761	Aab09761 IGFBP-2 I
9	93	94.9	47	3	AAB09628	Aab09628 Insulin 1
10	93	94.9	47	3	AAB09668	Aab09668 IGFBP-2 I
11	93	94.9	52	3	AAB09660	Aab09660 IGFBP-2 I
12	93	94.9	53	3	AAB09659	Aab09659 IGFBP-2 I

13	93	94.9	54	3	AAB09658	Aab09658	IGFBP-2	I
14	93	94.9	54	3	AAB09657	Aab09657	IGFBP-2	I
15	93	94.9	55	3	AAB09661	Aab09661	IGFBP-2	I
16	93	94.9	55	3	AAB09655	Aab09655	IGFBP-2	I
17	93	94.9	55	3	AAB09656	Aab09656	IGFBP-2	I
18	93	94.9	56	3	AAB09653	Aab09653	IGFBP-2	I
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22	93	94.9	57	3	AAB09651	Aab09651	IGFBP-2	I
23	93	94.9	58	3	AAB09649	Aab09649	IGFBP-2	I
24	93	94.9	58	3	AAB09650	Aab09650	IGFBP-2	I
25	93	94.9	59	3	AAB09647	Aab09647	IGFBP-2	I
26	93	94.9	59	3	AAB09648	Aab09648	IGFBP-2	I
27	93	94.9	59	3	AAB09663	Aab09663	IGFBP-2	I
28	93	94.9	60	3	AAB09645	Aab09645	IGFBP-2	I
29	93	94.9	60	3	AAB09646	Aab09646	IGFBP-2	I
30	93	94.9	61	3	AAB09643	Aab09643	IGFBP-2	I
31	93	94.9	61	3	AAB09664	Aab09664	IGFBP-2	I
32	93	94.9	61	3	AAB09644	Aab09644	IGFBP-2	I
33	93	94.9	62	3	AAB09641	Aab09641	IGFBP-2	I
34	93	94.9	62	3	AAB09642	Aab09642	IGFBP-2	I
35	93	94.9	63	3	AAB09639	Aab09639	IGFBP-2	I
36	93	94.9	63	3	AAB09640	Aab09640	IGFBP-2	I
37	93	94.9	64	3	AAB09638	Aab09638	IGFBP-2	I
38	93	94.9	64	3	AAB09637	Aab09637	IGFBP-2	I
39	93	94.9	64	3	AAB09627	Aab09627	Insulin	1
40	93	94.9	64	3	AAB09665	Aab09665	IGFBP-2	I
41	93	94.9	65	3	AAB09636	Aab09636	IGFBP-2	I
42	93	94.9	65	3	AAB09635	Aab09635	IGFBP-2	I
43	93	94.9	66	3	AAB09633	Aab09633	IGFBP-2	I
44	93	94.9	66	3	AAB09634	Aab09634	IGFBP-2	I
45	93	94.9	67	3	AAB09632	Aab09632	IGFBP-2	I
46	93	94.9	76	3	AAB09624	Aab09624	Insulin	1
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48	93	94.9	101	3	AAB09626	Aab09626	Insulin	1
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50	93	94.9	105	9	AED74029	Aed74029	Human pla	
51	93	94.9	123	2	AAY25505	Aay25505	Insulin-1	
52	93	94.9	139	3	AAB09625	Aab09625	Insulin	1
53	93	94.9	139	3	AAB09666	Aab09666	IGFBP-2	I
54	93	94.9	216	5	ABP41894	Abp41894	Human ova	
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58	93	94.9	289	3	AAB09753	Aab09753	IGFBP-2	a
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77	93	94.9	328	6	ABU56585	Abu56585 Lung canc
78	93	94.9	328	7	ADD14079	Add14079 Human src
79	93	94.9	328	7	ADE56686	Ade56686 Human Pro
80	93	94.9	328	7	ADE56682	Ade56682 Human Pro
81	93	94.9	328	7	ADJ68290	Adj68290 Human hea
82	93	94.9	328	7	ADN95269	Adn95269 Human BEC
83	93	94.9	328	8	ADK70455	Adk70455 Respirato
84	93	94.9	328	8	ADL61308	Adl61308 Human ins
85	93	94.9	328	8	ADQ20663	Adq20663 Human sof
86	93	94.9	328	8	ADQ26071	Adq26071 Insulin-1
87	93	94.9	328	9	ADY54943	Ady54943 Chronic v
88	93	94.9	328	9	ADZ87324	Adz87324 Human IGF
89	93	94.9	328	9	AEA47743	Aea47743 Amino aci
90	93	94.9	328	9	AEB29751	Aeb29751 Human ins
91	93	94.9	328	9	AED51292	Aed51292 Human ins
92	93	94.9	367	8	ADR66715	Adr66715 Human pro
93	93	94.9	367	8	ADR66373	Adr66373 Human pro
94	88	89.8	18	8	ADI29061	Adi29061 Human ins
95	88	89.8	34	3	AAB09733	Aab09733 IGFBP-2 I
96	87	88.8	18	8	ADI29063	Adi29063 Human ins
97	87	88.8	18	8	ADI29064	Adi29064 Human ins
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103	67	68.4	30	3	AAB09729	Aab09729 IGFBP-2 I
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105	63	64.3	29	3	AAB09728	Aab09728 IGFBP-2 I
106	63	64.3	30	3	AAB09630	Aab09630 Insulin 1
107	63	64.3	41	3	AAB09629	Aab09629 Insulin 1
108	63	64.3	41	3	AAB09669	Aab09669 IGFBP-2 I
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112	54	55.1	14	7	ADO32208	Ado32208 Peptide o
113	54	55.1	14	8	ADO07254	Ado07254 Peptide B
114	54	55.1	14	8	ADS74123	Ads74123 Peptide B
115	53	54.1	10	3	AAB09767	Aab09767 IGFBP-2 I
116	53	54.1	27	3	AAB09726	Aab09726 IGFBP-2 I
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119	47	48.0	51	4	AAB48120	Aab48120 Consensus
120	46	46.9	23	8	ADI29052	Adi29052 Human ins
121	46	46.9	52	3	AAB09674	Aab09674 IGFBP-1 I
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123	46	46.9	94	8	ADS18324	Ads18324 Human IGF
124	46	46.9	118	2	AYA25504	Aay25504 Insulin-1
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127	46	46.9	234	3	AAB09617	Aab09617 Insulin 1
128	46	46.9	258	1	AAP93154	Aap93154 Insulin-1
129	46	46.9	259	1	AAP91868	Aap91868 Recombina
130	46	46.9	259	6	ABB82754	Abb82754 Human IGF
131	46	46.9	259	6	ABB82757	Abb82757 Human IGF
132	46	46.9	259	8	ADE76944	Ade76944 Human pro
133	46	46.9	259	8	ADH17058	Adh17058 Human ins
134	46	46.9	259	8	ADL12500	Adl12500 Human ste

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:03:03 ; Search time 34.5 Seconds
 (without alignments)
 45.668 Million cell updates/sec

Title: US-10-519-890-16
 Perfect score: 98
 Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	93	94.9	328	2	US-09-253-316-28	Sequence 28, Appl
2	93	94.9	328	2	US-09-961-403-2	Sequence 2, Appl
3	93	94.9	328	7	5212074-4	Patent No. 5212074
4	54	55.1	14	2	US-10-215-759-14	Sequence 14, Appl
5	54	55.1	14	2	US-10-264-672-14	Sequence 14, Appl
6	54	55.1	14	2	US-10-383-999-14	Sequence 14, Appl
7	46	46.9	259	2	US-09-253-316-27	Sequence 27, Appl
8	46	46.9	259	2	US-09-976-594-229	Sequence 229, App
9	46	46.9	259	2	US-09-919-039-109	Sequence 109, App
10	46	46.9	259	2	US-09-949-001-17	Sequence 17, Appl
11	46	46.9	259	7	5212074-3	Patent No. 5212074
12	46	46.9	314	2	US-09-949-001-23	Sequence 23, Appl
13	43	43.9	301	2	US-09-543-681A-7708	Sequence 7708, Ap
14	42	42.9	170	2	US-09-902-540-11882	Sequence 11882, A
15	42	42.9	1642	1	US-08-447-411-45	Sequence 45, Appl

16	42	42.9	1642	1	US-08-662-227-2	Sequence 2, Appli
17	42	42.9	1642	2	US-09-017-947-2	Sequence 2, Appli
18	42	42.9	1642	2	US-09-925-442-2	Sequence 2, Appli
19	42	42.9	1648	1	US-08-662-227-35	Sequence 35, Appli
20	42	42.9	1648	2	US-09-017-947-35	Sequence 35, Appli
21	42	42.9	1648	2	US-09-925-442-35	Sequence 35, Appli
22	41	41.8	298	2	US-09-248-796A-18012	Sequence 18012, A
23	41	41.8	522	2	US-09-543-681A-5830	Sequence 5830, Ap
24	41	41.8	2079	2	US-09-949-016-8301	Sequence 8301, Ap
25	40	40.8	92	2	US-09-673-395A-285	Sequence 285, App
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27	40	40.8	227	2	US-09-225-366-4	Sequence 4, Appli
28	40	40.8	1651	1	US-08-447-411-2	Sequence 2, Appli
29	39	39.8	237	7	5212074-7	Patent No. 5212074
30	39	39.8	258	2	US-09-949-016-6093	Sequence 6093, Ap
31	39	39.8	287	2	US-09-949-016-9099	Sequence 9099, Ap
32	39	39.8	317	2	US-09-949-016-8185	Sequence 8185, Ap
33	39	39.8	337	2	US-09-902-540-16643	Sequence 16643, A
34	39	39.8	395	2	US-09-198-452A-790	Sequence 790, App
35	39	39.8	397	2	US-09-438-185A-742	Sequence 742, App
36	39	39.8	400	2	US-09-270-767-44593	Sequence 44593, A
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39	39	39.8	1603	2	US-09-949-016-6136	Sequence 6136, Ap
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55	38	38.8	317	2	US-08-473-089-27	Sequence 27, Appli
56	38	38.8	317	2	US-08-473-089-41	Sequence 41, Appli
57	38	38.8	317	2	US-08-473-089-47	Sequence 47, Appli
58	38	38.8	317	2	US-08-487-072A-27	Sequence 27, Appli
59	38	38.8	317	2	US-08-487-072A-41	Sequence 41, Appli
60	38	38.8	317	2	US-08-487-072A-47	Sequence 47, Appli
61	38	38.8	317	2	US-09-538-092-1009	Sequence 1009, Ap
62	38	38.8	317	3	US-10-329-258-4	Sequence 4, Appli
63	38	38.8	378	1	US-08-707-793A-4	Sequence 4, Appli
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65	38	38.8	434	2	US-09-538-092-103	Sequence 103, App
66	38	38.8	495	2	US-09-252-991A-19330	Sequence 19330, A
67	38	38.8	524	2	US-09-248-796A-20498	Sequence 20498, A
68	38	38.8	619	2	US-09-457-040B-9	Sequence 9, Appli
69	38	38.8	622	2	US-09-270-767-46333	Sequence 46333, A
70	38	38.8	865	2	US-09-417-197-111	Sequence 111, App
71	38	38.8	871	2	US-09-417-197-109	Sequence 109, App
72	38	38.8	919	1	US-08-788-674-4	Sequence 4, Appli
73	38	38.8	951	2	US-08-816-346-58	Sequence 58, Appli
74	38	38.8	951	2	US-09-335-411-58	Sequence 58, Appli
75	38	38.8	952	1	US-08-788-674-5	Sequence 5, Appli
76	38	38.8	952	2	US-08-816-346-4	Sequence 4, Appli

77	38	38.8	952	2	US-09-335-411-4	Sequence 4, Appli
78	38	38.8	967	2	US-08-816-346-56	Sequence 56, Appl
79	38	38.8	967	2	US-09-335-411-56	Sequence 56, Appl
80	38	38.8	968	2	US-08-816-346-2	Sequence 2, Appli
81	38	38.8	968	2	US-09-335-411-2	Sequence 2, Appli
82	37.5	38.3	165	2	US-09-489-039A-9882	Sequence 9882, Ap
83	37	37.8	132	2	US-09-732-210-1687	Sequence 1687, Ap
84	37	37.8	134	2	US-09-489-039A-12144	Sequence 12144, A
85	37	37.8	156	2	US-09-270-767-35189	Sequence 35189, A
86	37	37.8	156	2	US-09-270-767-50406	Sequence 50406, A
87	37	37.8	170	2	US-09-775-925-32	Sequence 32, Appl
88	37	37.8	201	2	US-09-570-214B-13	Sequence 13, Appl
89	37	37.8	241	2	US-09-775-925-8	Sequence 8, Appli
90	37	37.8	323	2	US-09-619-353-6	Sequence 6, Appli
91	37	37.8	345	2	US-09-543-681A-6792	Sequence 6792, Ap
92	37	37.8	394	2	US-09-270-767-41967	Sequence 41967, A
93	37	37.8	476	2	US-09-328-352-5950	Sequence 5950, Ap
94	37	37.8	483	2	US-09-252-991A-32383	Sequence 32383, A
95	37	37.8	483	2	US-09-385-219A-48	Sequence 48, Appl
96	37	37.8	509	2	US-09-955-732A-14	Sequence 14, Appl
97	37	37.8	509	2	US-09-775-925-6	Sequence 6, Appli
98	37	37.8	548	2	US-09-543-681A-6561	Sequence 6561, Ap
99	37	37.8	820	1	US-08-380-182-23	Sequence 23, Appl
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102	37	37.8	1163	2	US-09-949-016-11047	Sequence 11047, A
103	36	36.7	63	2	US-09-621-976-5664	Sequence 5664, Ap
104	36	36.7	64	2	US-09-513-999C-4670	Sequence 4670, Ap
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106	36	36.7	126	2	US-09-134-001C-3038	Sequence 3038, Ap
107	36	36.7	134	2	US-09-710-279-2842	Sequence 2842, Ap
108	36	36.7	137	2	US-09-270-767-40132	Sequence 40132, A
109	36	36.7	137	2	US-09-270-767-55348	Sequence 55348, A
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118	36	36.7	194	5	PCT-US95-10194-9	Sequence 9, Appli
119	36	36.7	198	2	US-09-489-039A-7717	Sequence 7717, Ap
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133	36	36.7	427	2	US-09-902-540-15261	Sequence 15261, A
134	36	36.7	463	1	US-08-162-402B-9	Sequence 9, Appli
135	36	36.7	549	2	US-09-248-796A-20854	Sequence 20854, A
136	36	36.7	562	2	US-09-252-991A-30993	Sequence 30993, A
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OM protein - protein search, using sw model

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 (without alignments)
 85.517 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	93	94.9	228	3	US-09-925-301-1061	Sequence 1061, Ap
4	93	94.9	328	3	US-09-961-403-2	Sequence 2, Appli
5	93	94.9	328	4	US-10-011-859-28	Sequence 28, Appl
6	93	94.9	328	4	US-10-408-765A-96	Sequence 96, Appl
7	93	94.9	328	4	US-10-648-593-232	Sequence 232, App
8	93	94.9	328	4	US-10-706-791-9	Sequence 9, Appli
9	93	94.9	328	5	US-10-723-860-3483	Sequence 3483, Ap
10	93	94.9	328	5	US-10-991-321-28	Sequence 28, Appl
11	93	94.9	328	5	US-10-923-035-36	Sequence 36, Appl
12	93	94.9	328	5	US-10-887-229A-4	Sequence 4, Appli
13	93	94.9	328	5	US-10-756-149-5613	Sequence 5613, Ap
14	93	94.9	328	5	US-10-501-035-268	Sequence 268, App
15	93	94.9	328	6	US-11-149-564-28	Sequence 28, Appl
16	93	94.9	328	6	US-11-169-041-227	Sequence 227, App

17	93	94.9	328	6	US-11-072-175-232	Sequence 232, App
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20	54	55.1	14	4	US-10-264-672-14	Sequence 14, Appl
21	54	55.1	14	4	US-10-383-999-14	Sequence 14, Appl
22	54	55.1	14	6	US-11-031-919-14	Sequence 14, Appl
23	46	46.9	94	4	US-10-400-005-4	Sequence 4, Appli
24	46	46.9	259	3	US-09-919-039-109	Sequence 109, App
25	46	46.9	259	4	US-10-011-859-27	Sequence 27, Appl
26	46	46.9	259	4	US-10-440-464-57	Sequence 57, Appl
27	46	46.9	259	4	US-10-706-791-7	Sequence 7, Appli
28	46	46.9	259	4	US-10-400-005-1	Sequence 1, Appli
29	46	46.9	259	5	US-10-893-315-65	Sequence 65, Appl
30	46	46.9	259	5	US-10-887-229A-2	Sequence 2, Appli
31	46	46.9	259	5	US-10-756-149-5095	Sequence 5095, Ap
32	46	46.9	259	5	US-10-821-234-1561	Sequence 1561, Ap
33	46	46.9	259	6	US-11-149-564-27	Sequence 27, Appl
34	46	46.9	314	5	US-10-893-315-99	Sequence 99, Appl
35	45	45.9	5317	4	US-10-668-767-59	Sequence 59, Appl
36	44	44.9	88	3	US-09-764-891-3371	Sequence 3371, Ap
37	44	44.9	88	4	US-10-091-572-259	Sequence 259, App
38	44	44.9	711	4	US-10-424-599-259955	Sequence 259955,
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41	43	43.9	407	4	US-10-369-493-13871	Sequence 13871, A
42	43	43.9	638	4	US-10-425-115-314451	Sequence 314451,
43	43	43.9	652	4	US-10-425-114-59143	Sequence 59143, A
44	43	43.9	1338	4	US-10-257-021-30	Sequence 30, Appl
45	43	43.9	1374	4	US-10-291-172-682	Sequence 682, App
46	43	43.9	1374	4	US-10-221-278-682	Sequence 682, App
47	43	43.9	1381	4	US-10-291-172-306	Sequence 306, App
48	43	43.9	1381	4	US-10-221-278-306	Sequence 306, App
49	43	43.9	1381	4	US-10-381-792-1	Sequence 1, Appli
50	43	43.9	1805	4	US-10-287-226-316	Sequence 316, App
51	43	43.9	1823	4	US-10-381-792-2	Sequence 2, Appli
52	42.5	43.4	198	4	US-10-369-493-13897	Sequence 13897, A
53	42	42.9	39	4	US-10-425-115-231462	Sequence 231462,
54	42	42.9	437	5	US-10-450-763-51171	Sequence 51171, A
55	42	42.9	1642	3	US-09-925-442-2	Sequence 2, Appli
56	42	42.9	1642	5	US-10-884-813-4	Sequence 4, Appli
57	42	42.9	1648	3	US-09-925-442-35	Sequence 35, Appl
58	41	41.8	134	4	US-10-425-115-366288	Sequence 366288,
59	41	41.8	284	5	US-10-501-282-1226	Sequence 1226, Ap
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61	41	41.8	428	4	US-10-425-114-45760	Sequence 45760, A
62	41	41.8	451	4	US-10-424-599-173619	Sequence 173619,
63	41	41.8	480	4	US-10-282-122A-68494	Sequence 68494, A
64	41	41.8	2115	4	US-10-208-948-4	Sequence 4, Appli
65	41	41.8	4493	5	US-10-704-781-3	Sequence 3, Appli
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93	40	40.8	2505	4	US-10-205-331-20	Sequence 20, Appl
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96	39.5	40.3	104	4	US-10-425-115-263379	Sequence 263379,
97	39.5	40.3	333	6	US-11-097-143-5829	Sequence 5829, Ap
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107	39	39.8	183	4	US-10-425-114-37326	Sequence 37326, A
108	39	39.8	188	4	US-10-282-122A-49027	Sequence 49027, A
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116	39	39.8	258	4	US-10-435-696-47	Sequence 47, Appl
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119	39	39.8	275	4	US-10-437-963-106582	Sequence 106582,
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129	39	39.8	428	4	US-10-649-852-36	Sequence 36, Appl
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132	39	39.8	479	4	US-10-425-114-56543	Sequence 56543, A
133	39	39.8	511	5	US-10-450-763-34370	Sequence 34370, A
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135	39	39.8	549	4	US-10-425-115-296906	Sequence 296906,
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OM protein - protein search, using sw model

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 45.998 Million cell updates/sec

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5	39	39.8	564	6	US-10-449-902-52967	Sequence 52967, A
6	39	39.8	604	6	US-10-953-349-7849	Sequence 7849, Ap
7	39	39.8	623	6	US-10-953-349-7848	Sequence 7848, Ap
8	39	39.8	675	6	US-10-953-349-7847	Sequence 7847, Ap
9	38	38.8	207	7	US-11-197-712-386	Sequence 386, App
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13	38	38.8	624	6	US-10-449-902-54158	Sequence 54158, A
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33	36	36.7	640	6	US-10-953-349-40224	Sequence 40224, A
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35	36	36.7	661	6	US-10-449-902-51012	Sequence 51012, A
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37	36	36.7	697	6	US-10-953-349-40222	Sequence 40222, A
38	36	36.7	746	6	US-10-953-349-2717	Sequence 2717, Ap
39	36	36.7	772	6	US-10-953-349-2716	Sequence 2716, Ap
40	36	36.7	829	6	US-10-953-349-2715	Sequence 2715, Ap
41	35.5	36.2	186	6	US-10-953-349-25121	Sequence 25121, A
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43	35.5	36.2	302	6	US-10-953-349-25119	Sequence 25119, A
44	35.5	36.2	402	7	US-11-289-102-218	Sequence 218, App
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46	35	35.7	164	7	US-11-315-825-29	Sequence 29, Appl
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56	35	35.7	295	6	US-10-953-349-18040	Sequence 18040, A
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58	35	35.7	334	6	US-10-953-349-18918	Sequence 18918, A
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65	35	35.7	503	6	US-10-449-902-45896	Sequence 45896, A
66	35	35.7	553	7	US-11-165-586-26	Sequence 26, Appl
67	35	35.7	632	6	US-10-449-902-56080	Sequence 56080, A
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74	35	35.7	711	6	US-10-449-902-49517	Sequence 49517, A
75	35	35.7	737	6	US-10-196-749-38	Sequence 38, Appl

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77	35	35.7	737	7	US-11-296-155-15	Sequence 15, Appl
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80	34.5	35.2	343	6	US-10-953-349-834	Sequence 834, App
81	34.5	35.2	360	6	US-10-953-349-833	Sequence 833, App
82	34.5	35.2	900	6	US-10-839-442A-22	Sequence 22, Appl
83	34	34.7	164	6	US-10-953-349-25534	Sequence 25534, A
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88	34	34.7	229	6	US-10-449-902-29327	Sequence 29327, A
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91	34	34.7	262	6	US-10-953-349-38302	Sequence 38302, A
92	34	34.7	266	6	US-10-953-349-38301	Sequence 38301, A
93	34	34.7	272	7	US-11-105-233-168	Sequence 168, App
94	34	34.7	291	7	US-11-301-554-333	Sequence 333, App
95	34	34.7	292	6	US-10-953-349-38300	Sequence 38300, A
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103	34	34.7	541	6	US-10-449-902-47025	Sequence 47025, A
104	34	34.7	599	6	US-10-449-902-41572	Sequence 41572, A
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107	34	34.7	639	6	US-10-449-902-55962	Sequence 55962, A
108	34	34.7	657	6	US-10-449-902-40797	Sequence 40797, A
109	34	34.7	698	6	US-10-449-902-46109	Sequence 46109, A
110	34	34.7	728	6	US-10-449-902-42713	Sequence 42713, A
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112	34	34.7	735	6	US-10-196-749-88	Sequence 88, Appl
113	34	34.7	757	6	US-10-536-440-3	Sequence 3, Appli
114	34	34.7	806	6	US-10-449-902-43949	Sequence 43949, A
115	34	34.7	831	6	US-10-449-902-51780	Sequence 51780, A
116	34	34.7	885	6	US-10-449-902-47114	Sequence 47114, A
117	33.5	34.2	63	6	US-10-449-902-35108	Sequence 35108, A
118	33.5	34.2	182	6	US-10-449-902-51584	Sequence 51584, A
119	33.5	34.2	327	6	US-10-953-349-5068	Sequence 5068, Ap
120	33.5	34.2	388	6	US-10-953-349-5067	Sequence 5067, Ap
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123	33.5	34.2	502	6	US-10-953-349-5066	Sequence 5066, Ap
124	33.5	34.2	505	6	US-10-953-349-5432	Sequence 5432, Ap
125	33.5	34.2	548	6	US-10-449-902-47226	Sequence 47226, A
126	33.5	34.2	1357	6	US-10-449-902-49437	Sequence 49437, A
127	33	33.7	17	7	US-11-134-871-441	Sequence 441, App
128	33	33.7	53	6	US-10-471-571A-3836	Sequence 3836, Ap
129	33	33.7	125	6	US-10-953-349-39597	Sequence 39597, A
130	33	33.7	127	6	US-10-953-349-6937	Sequence 6937, Ap
131	33	33.7	189	6	US-10-449-902-42125	Sequence 42125, A
132	33	33.7	218	6	US-10-953-349-39596	Sequence 39596, A
133	33	33.7	220	6	US-10-953-349-6936	Sequence 6936, Ap
134	33	33.7	230	6	US-10-953-349-39595	Sequence 39595, A
135	33	33.7	240	6	US-10-953-349-6935	Sequence 6935, Ap
136	33	33.7	247	7	US-11-197-712-346	Sequence 346, App

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:44 ; Search time 18.75 Seconds
 (without alignments)
 92.368 Million cell updates/sec

Title: US-10-519-890-16

Perfect score: 98

Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	93	94.9	304	2	A33274	insulin-like growth
2	93	94.9	310	2	A60967	insulin-like growth
3	93	94.9	317	2	I46916	insulin-like growth
4	93	94.9	328	1	A41927	insulin-like growth
5	87	88.8	305	2	JN0508	insulin-like growth
6	87	88.8	305	2	I48601	insulin-like growth
7	48	49.0	236	2	T45067	hypothetical protein
8	48	49.0	272	1	A36082	insulin-like growth
9	47	48.0	263	1	S23009	insulin-like growth
10	46	46.9	259	1	IOHU1	insulin-like growth
11	45	45.9	272	2	I48600	insulin-like growth
12	42	42.9	334	2	A83991	glycolate oxidase
13	42	42.9	1642	2	I51018	cobra venom factor
14	41	41.8	299	2	AH0367	conserved hypothetical
15	41	41.8	830	2	T04848	protein kinase homolog
16	41	41.8	2143	2	G96595	hypothetical protein
17	40	40.8	227	2	JQ1945	nucleoside-triphosphatase
18	40	40.8	949	2	A81138	exonuclease ABC c

19	40	40.8	949	2	E75352	glycine cleavage s
20	40	40.8	1651	1	C3NJ	complement C3 prec
21	40	40.8	2505	1	XYRTFA	enoyl-[acyl-carri
22	39.5	40.3	444	2	E96905	TPR-repeat-contain
23	39.5	40.3	1557	2	T28811	hypothetical prote
24	39	39.8	214	2	JQ2001	hypothetical 24K p
25	39	39.8	237	2	I47031	insulin-like growt
26	39	39.8	254	2	I48603	insulin-like growt
27	39	39.8	254	2	I48599	insulin-like growt
28	39	39.8	254	2	JC1464	insulin-like growt
29	39	39.8	258	1	B37252	insulin-like growt
30	39	39.8	258	2	A45403	insulin-like growt
31	39	39.8	353	2	D96596	hypothetical prote
32	39	39.8	395	2	A86583	aromatic AA aminot
33	39	39.8	395	2	B72042	aromatic-amino-acid
34	39	39.8	419	2	G86198	hypothetical prote
35	39	39.8	456	2	F88493	protein F57B9.9 [i
36	39	39.8	522	2	S33029	hypothetical prote
37	39	39.8	542	2	B81662	apolipoprotein N-a
38	39	39.8	619	2	E82765	DNA mismatch repai
39	39	39.8	879	2	B84765	hypothetical prote
40	39	39.8	915	1	A48225	subtilisin-like pr
41	39	39.8	915	2	B48225	probable proprotei
42	39	39.8	1239	1	VHWVEE	structural polypro
43	39	39.8	1240	1	VHWVEV	structural polypro
44	39	39.8	1241	2	S26373	genome polyprotein
45	39	39.8	1242	2	A56605	structural polypro
46	39	39.8	1242	2	S72350	structural polypro
47	39	39.8	1256	2	S14556	asparagine-rich pr
48	39	39.8	1403	2	T49093	hypothetical prote
49	39	39.8	1548	2	S34583	serine proteinase
50	39	39.8	1603	2	S23810	collagen alpha 1(X
51	39	39.8	2895	2	T08437	hyperplastic discs
52	38.5	39.3	132	2	D72616	hypothetical prote
53	38.5	39.3	333	1	H86381	probable acid phos
54	38	38.8	317	2	S45054	GTP-binding regula
55	38	38.8	317	2	S38398	GTP-binding regula
56	38	38.8	317	2	A33928	GTP-binding protei
57	38	38.8	317	2	B33928	GTP-binding protei
58	38	38.8	317	2	A36986	activated protein
59	38	38.8	344	2	T37277	probable cathepsin
60	38	38.8	362	2	S71071	site-specific DNA-
61	38	38.8	428	2	A83494	hypothetical prote
62	38	38.8	434	2	S67639	26S proteasome reg
63	38	38.8	465	2	F65207	hydH protein - Esc
64	38	38.8	484	2	T16695	hypothetical prote
65	38	38.8	618	2	I48914	protein-tyrosine k
66	38	38.8	619	2	A44266	protein-tyrosine k
67	38	38.8	624	2	T48587	peptide transporte
68	38	38.8	647	2	A37086	beta-galactosidase
69	38	38.8	803	2	T24685	hypothetical prote
70	38	38.8	846	2	T39261	amp deaminase - fi
71	38	38.8	919	2	S33942	hexon protein - hu
72	38	38.8	923	1	HXAD40	hexon protein - hu
73	38	38.8	925	1	HXAD41	hexon protein - hu
74	38	38.8	936	2	S57637	hexon protein - hu
75	38	38.8	937	2	S55504	hexon protein - hu
76	38	38.8	937	2	S39301	hexon protein - hu
77	38	38.8	940	2	S37216	hexon protein - hu
78	38	38.8	942	2	S39298	hexon protein - hu
79	38	38.8	952	1	HXAD5	hexon protein - hu

80	38	38.8	967	1	HXAD2	hexon protein - hu
81	38	38.8	996	2	T10725	protein kinase Xa2
82	38	38.8	1286	2	T18734	hypothetical prote
83	38	38.8	1434	2	C82923	DNA-directed RNA p
84	37.5	38.3	264	2	AI0439	conserved hypothet
85	37.5	38.3	404	2	S12209	pectate lyase (EC
86	37.5	38.3	3133	2	S52093	hemocytin - silkwo
87	37	37.8	33	2	A55998	brevinin-2Ea - edi
88	37	37.8	117	2	F70074	hypothetical prote
89	37	37.8	132	2	T38486	probable ribosomal
90	37	37.8	134	2	H84726	hypothetical prote
91	37	37.8	145	2	S36244	fimA protein - Bor
92	37	37.8	207	2	E90140	hypothetical prote
93	37	37.8	236	2	AF2927	transcription regu
94	37	37.8	262	2	A98355	transcription regu
95	37	37.8	363	2	C83128	2,3-butanediol deh
96	37	37.8	394	2	D69370	probable acyl-CoA
97	37	37.8	465	2	T29257	hypothetical prote
98	37	37.8	477	2	AC0903	Penicillin-binding
99	37	37.8	477	2	H85981	D-alanyl-D-alanine
100	37	37.8	477	2	E91136	D-alanyl-D-alanine
101	37	37.8	477	2	A54535	serine-type D-Ala-
102	37	37.8	482	2	AC0426	serine-type D-Ala-
103	37	37.8	554	2	E97852	hypothetical prote
104	37	37.8	602	2	H86468	protein F12K21.20
105	37	37.8	604	2	F87244	replicative DNA he
106	37	37.8	608	2	D72306	hypothetical prote
107	37	37.8	707	2	T28418	ORF MSV257 leucine
108	37	37.8	819	2	AH0056	aspartate kinase (
109	37	37.8	820	1	DEECK	thrA bifunctional
110	37	37.8	820	2	B85480	aspartokinase I, h
111	37	37.8	820	2	B90629	aspartokinase I-ho
112	37	37.8	820	2	AC0502	aspartokinase I/h0
113	37	37.8	1018	2	T43168	hypothetical prote
114	37	37.8	1139	2	T33368	hypothetical prote
115	37	37.8	1158	2	S57348	nuclear factor RIP
116	37	37.8	1217	2	T00607	hypothetical prote
117	37	37.8	1259	2	T16038	hypothetical prote
118	37	37.8	1282	2	T30577	DNA topoisomerase
119	37	37.8	5126	2	S40450	ryanodine receptor
120	36.5	37.2	125	2	F64685	hypothetical prote
121	36.5	37.2	125	2	A71831	hypothetical prote
122	36.5	37.2	229	2	B69712	mutants block spor
123	36.5	37.2	359	1	ADRFAS	fructose-bisphosph
124	36.5	37.2	403	2	JC5269	neuron-specific si
125	36	36.7	71	2	AG0507	conserved hypothet
126	36	36.7	118	2	D89951	50S ribosomal prot
127	36	36.7	148	2	T28287	ORF MSV126 hypothe
128	36	36.7	150	2	A95197	conserved hypothet
129	36	36.7	150	2	F98063	hypothetical prote
130	36	36.7	173	2	T06103	hypothetical prote
131	36	36.7	186	2	AI3292	protein translatio
132	36	36.7	211	2	C83360	hypothetical prote
133	36	36.7	232	2	C83139	outer membrane pro
134	36	36.7	249	2	JC6191	ATP-binding casset
135	36	36.7	262	2	B90099	hypothetical prote
136	36	36.7	265	1	MNVNIM	nonstructural prot
137	36	36.7	265	1	MNVNV4	nonstructural prot
138	36	36.7	273	2	PC4153	monophenol monooxy
139	36	36.7	283	2	T26448	hypothetical prote
140	36	36.7	286	2	B95011	hypothetical prote